**Amendments to the Specification:**

On page 6, please **replace** the first two paragraphs with the following single paragraph:

**Figure 6.** ~~Gene expression profiles of ventral and dorsal pharyngeal endoderm in E7.5 mouse embryo. Gray area shows the gene expression of both sides at small level. Red lines indicate a five fold increase in expression and blue lines indicate a five fold decrease in expression.~~

~~**Figure 7.**~~ Whole mount *in situ* hybridization confirmed a microarray data suggested a gene differential expressed between ventral and dorsal midline of pharyngeal endoderm.

On pages 21-22, please **replace** the three paragraphs beginning on page 21 line 26 and running through page 22 line 32 with the following three paragraphs:

*Gene expression profiles and the analysis of our microarray data.* Our interest in ventral pharyngeal development has led us to ask whether the ventral pharyngeal endoderm differentially expresses messages as compared to the dorsal pharyngeal endoderm. This inquiry lends itself to laser capture microdissection and microarray screening. Laser capture microdissection was performed on fresh frozen sections from day 8.5 mouse embryos. The regions targeted for comparison were dorsal midline versus ventral midline foregut endoderm. Figure 4 shows the steps in the capture of the ventral endoderm. RNA was extracted and cDNA prepared by the method described in the methods section of this application. The gene profiles of the GeneSpring data analysis platform provides systems operation, instrument control and data analysis for the entire genechip. It automatically acquires and processes hybridization data, analyzes algorithms and then allows review, comparison, graphing, filtration, analysis and reporting in different modes. Every sample has its own expression profile database. All the comparison and subtraction analyses are performed by the software. ~~A two-fold~~

~~differential expression of genes is listed and sorted gene tree based on gene function or family showed as **Figure 6** of the profiles of ventral and dorsal pharyngeal endoderm.~~

**Figure 5A** shows a pilot test to determine the number of cycles needed for long distance PCR amplification of the cDNA pools. The highly abundant housekeeping gene GAPDH A was chosen to perform quantitative real time PCR on cDNA generated from the microdissected cells of the dorsal and ventral midline of the pharyngeal endoderm. The linear range or log phase of the amplification is between cycles 20–28 as indicated by the arrows. **Figure 5B** shows 2 $\mu$l of reverse transcription product from laser microdissected cells of the ventral and dorsal midline of the pharyngeal endoderm, used to perform long distance PCR at 25 and 30 cycles. The amplified pools of cDNA are uniformly distributed in a smear between 100bp to 6000bp as shown in the agarose gel. These data indicated that 30 cycles of PCR caused over-amplification of the cDNA pool. The products from 25 cycles of amplification were used for continuing microarray analysis.

~~**Figure 7**~~ **Figure 6** shows that whole mount *in situ* hybridization confirmed microarray data suggesting differential gene expression between the ventral and dorsal midline of pharyngeal endoderm. **Figure 6A:** ~~**Figure 7A**~~: DiI/CRSE injection in chick embryo stage 5 traced cells from the prechordal plate and generated the ventral midline of the pharyngeal endoderm at stage 12, but not the dorsal midline or other regions of the pharyngeal endoderm. **Figure 6B:** ~~**Figure 7B**~~: After DNA microarray analysis and comparison of the gene expression profiles, there are many genes differentially expressed between the dorsal and ventral midline of the pharyngeal endoderm. This figure shows one example which was indicated by the microarray data, and confirmed it by *in situ* hybridization in chick embryo at stage 12, in which this gene was highly and specifically expressed in the ventral midline but not the dorsal midline as arrow pointed.